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## PENDING CLAIMS:

- 8. A method for in vitro screening for a transdominant intracellular bioactive agent capable of altering the phenotype of a cell, said method comprising the steps:
  - a) introducing a molecular library of retroviral vectors comprising randomized candidate nucleic acids into a plurality of cells, wherein each of said nucleic acids comprises a different nucleotide sequence, wherein said randomized candidate nucleic acids are expressed in said cells to produce a plurality of randomized peptides, wherein each of said retroviral vectors comprises a nucleic acid encoding at least one glycine N-terminal to the randomized peptide;
  - b) screening said plurality of cells for a cell exhibiting an altered phenotype, wherein said altered phenotype is due to the presence of a transdominant bioactive agent; and
  - c) identifying said transdominant bioactive agent.
- 9. A method according to claim 8 wherein said identifying comprises:
  - i) isolating said cell exhibiting an altered phenotype.
- 10. A method according to claim 9 wherein said identifying further comprises:

  ii) sequencing said nucleic acid encoding said transdominant bioactive agent.
- 11. A method according to claim 8 wherein each of said nucleic acids further comprise a presentation sequence capable of presenting said expression product in a conformationally restricted form.
- 12. A method according to claim 8 wherein said cells are mammalian cells.
- 13. A method according to claim 8 wherein said library comprises at least 10<sup>4</sup> different nucleic acids.
- 14. A method according to claim 8 wherein said library comprises at least 10<sup>5</sup> different nucleic acids.
- 15. A method according to claim 8 wherein said library comprises at least 10<sup>6</sup> different nucleic acids.
- 16. A method according to claim 8 wherein said library comprises at least 10<sup>7</sup> different nucleic acids.
- 17. A method according to claim 8 wherein said library comprises at least 10<sup>8</sup> different nucleic acids.

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- 18. A method according to claim 8 wherein said library comprises at least 10<sup>9</sup> different nucleic acids.
- 19. A method according to claim 8 wherein each of said candidate nucleic acids is linked to nucleic acid encoding at least one fusion partner.
- 20. A method according to claim 19 wherein said fusion partner comprises a nuclear localization signal sequence.
- 21. A method for in vitro screening for a transdominant intracellular bioactive agent capable of altering the phenotype of a cell, said method comprising the steps:
  - a) introducing a molecular library of retroviral vectors comprising randomized candidate nucleic acids into a plurality of cells, wherein each of said nucleic acids comprises a different nucleotide sequence, wherein said randomized candidate nucleic acids are expressed in said cells to produce a plurality of randomized peptides;
  - b) screening said plurality of cells for a cell exhibiting an altered phenotype, wherein said altered phenotype is due to the presence of a transdominant bioactive agent, wherein said altered phenotype is cell growth; and
  - c) identifying said transdominant bioactive agent.
- 22. A method for in vitro screening for a transdominant intracellular bioactive agent capable of altering the phenotype of a cell, said method comprising the steps:
  - a) introducing a molecular library of retroviral vectors comprising randomized candidate nucleic acids into a plurality of cells, wherein each of said nucleic acids comprises a different nucleotide sequence, wherein said randomized candidate nucleic acids are expressed in said cells to produce a plurality of randomized peptides;
  - b) screening said plurality of cells for a cell exhibiting an altered phenotype, wherein said altered phenotype is due to the presence of a transdominant bioactive agent, wherein said altered phenotype is cell death; and
  - c) identifying said transdominant bioactive agent.
- 23. A method for in vitro screening for a transdominant intracellular bioactive agent capable of altering the phenotype of a cell, said method comprising the steps:
  - a) introducing a molecular library of retroviral vectors comprising randomized candidate nucleic acids into a plurality of cells, wherein each of said nucleic acids comprises a different nucleotide sequence, wherein said randomized candidate nucleic acids are expressed in said cells to produce a plurality of randomized peptides;
  - b) screening said plurality of cells for a cell exhibiting an altered phenotype, wherein said altered phenotype is due to the presence of a transdominant bioactive

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agent, wherein said altered phenotype is a change in expression of cellular differentiation markers; and

- c) identifying said transdominant bioactive agent.
- 24. The method according to claim 23, wherein said cellular differentiation markers are characteristic of T-cell activation.
- 25. The method according to claim 23, wherein said cellular differentiation markers are characteristic of B-cell activation.